09753385

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RAW SEQUENCE LISTING   DATE: 12/31/2002
PATENT APPLICATION: US/09/753,385   TIME: 14:15:22

Input Set : A:\10278-025004.TXT
Output Set: N:\CRF4\12312002\I753385.raw

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 4 <110> APPLICANT: Heartlein, Michael W.
 5          Lemontt, Jeffrey F.
 6          Concino, Michael F.
 8 <120> TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE IN TRANSPORT
 9          OF A SELECTED SUBSTANCE INTO CELLS
12 <130> FILE REFERENCE: 10278-025004
14 <140> CURRENT APPLICATION NUMBER: US 09/753,385
15 <141> CURRENT FILING DATE: 2002-12-10
17 <150> PRIOR APPLICATION NUMBER: US 08/470,058
18 <151> PRIOR FILING DATE: 1995-06-06
20 <150> PRIOR APPLICATION NUMBER: US 09/037,188
21 <151> PRIOR FILING DATE: 1998-03-09
23 <150> PRIOR APPLICATION NUMBER: US 09/285,310
24 <151> PRIOR FILING DATE: 1999-04-02
26 <160> NUMBER OF SEQ ID NOS: 12
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 3428
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (14)...(3235)
39 <400> SEQUENCE: 1
40 agaggctgcg agc atg ggg ccc tgg ggc tgg aaa ttg cgc tgg acc gtc        49
41              Met Gly Pro Trp Gly Trp Lys Leu Arg Trp Thr Val
42                1                5                     10
44 gcc ttg ctc ctc gcc gcg gcg ggg act gca gtg ggc gac aga tgt gaa      97
45 Ala Leu Leu Leu Ala Ala Ala Gly Thr Ala Val Gly Asp Arg Cys Glu
46          15                  20                  25
48 aga aac gag ttc cag tgc caa gac ggg aaa tgc atc tcc tac aag tgg     145
49 Arg Asn Glu Phe Gln Cys Gln Asp Gly Lys Cys Ile Ser Tyr Lys Trp
50      30                  35                  40
52 gtc tgc gat ggc agc gct gag tgc cag gat ggc tct gat gag tcc cag     193
53 Val Cys Asp Gly Ser Ala Glu Cys Gln Asp Gly Ser Asp Glu Ser Gln
54  45                  50                  55                  60
56 gag acg tgc ttg tct gtc acc tgc aaa tcc ggg gac ttc agc tgt ggg     241
57 Glu Thr Cys Leu Ser Val Thr Cys Lys Ser Gly Asp Phe Ser Cys Gly
58              65                  70                  75
60 ggc cgt gtc aac cgc tgc att cct cag ttc tgg agg tgc gat ggc caa     289
61 Gly Arg Val Asn Arg Cys Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln
62              80                  85                  90
64 gtg gac tgc gac aac ggc tca gac gag caa ggc tgt ccc ccc aag acg     337
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C--> 15 (line marked on page)

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65 Val Asp Cys Asp Asn Gly Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr
66          95              100             105
68 tgc tcc cag gac gag ttt cgc tgc cac gat ggg aag tgc atc tct cgg      385
69 Cys Ser Gln Asp Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg
70     110             115             120
72 cag ttc gtc tgt gac tca gac cgg gac tgc ttg gac ggc tca gac gag      433
73 Gln Phe Val Cys Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu
74 125             130             135             140
76 gcc tcc tgc ccg gtg ctc acc tgt ggt ccc gcc agc ttc cag tgc aac      481
77 Ala Ser Cys Pro Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn
78             145             150             155
80 agc tcc acc tgc atc ccc cag ctg tgg gcc tgc gac aac gac ccc gac      529
81 Ser Ser Thr Cys Ile Pro Gln Leu Trp Ala Cys Asp Asn Asp Pro Asp
82             160             165             170
84 tgc gaa gat ggc tcg gat gag tgg ccg cag cgc tgt agg ggt ctt tac      577
85 Cys Glu Asp Gly Ser Asp Glu Trp Pro Gln Arg Cys Arg Gly Leu Tyr
86         175             180             185
88 gtg ttc caa ggg gac agt agc ccc tgc tcg gcc ttc gag ttc cac tgc      625
89 Val Phe Gln Gly Asp Ser Ser Pro Cys Ser Ala Phe Glu Phe His Cys
90     190             195             200
92 cta agt ggc gag tgc atc cac tcc agc tgg cgc tgt gat ggt ggc ccc      673
93 Leu Ser Gly Glu Cys Ile His Ser Ser Trp Arg Cys Asp Gly Gly Pro
94 205             210             215             220
96 gac tgc aag gac aaa tct gac gag gaa aac tgc gct gtg gcc acc tgt      721
97 Asp Cys Lys Asp Lys Ser Asp Glu Glu Asn Cys Ala Val Ala Thr Cys
98             225             230             235
100 cgc cct gac gaa ttc cag tgc tct gat gga aac tgc atc cat ggc agc     769
101 Arg Pro Asp Glu Phe Gln Cys Ser Asp Gly Asn Cys Ile His Gly Ser
102             240             245             250
104 cgg cag tgt gac cgg gaa tat gac tgc aag gac atg agc gat gaa gtt     817
105 Arg Gln Cys Asp Arg Glu Tyr Asp Cys Lys Asp Met Ser Asp Glu Val
106         255             260             265
108 ggc tgc gtt aat gtg aca ctc tgc gag gga ccc aac aag ttc aag tgt     865
109 Gly Cys Val Asn Val Thr Leu Cys Glu Gly Pro Asn Lys Phe Lys Cys
110     270             275             280
112 cac agc ggc gaa tgc atc acc ctg gac aaa gtc tgc aac atg gct aga     913
113 His Ser Gly Glu Cys Ile Thr Leu Asp Lys Val Cys Asn Met Ala Arg
114 285             290             295             300
116 gac tgc cgg gac tgg tca gat gaa ccc atc aaa gag tgc ggg acc aac     961
117 Asp Cys Arg Asp Trp Ser Asp Glu Pro Ile Lys Glu Cys Gly Thr Asn
118             305             310             315
120 gaa tgc ttg gac aac aac ggc ggc tgt tcc cac gtc tgc aat gac ctt     1009
121 Glu Cys Leu Asp Asn Asn Gly Gly Cys Ser His Val Cys Asn Asp Leu
122             320             325             330
124 aag atc ggc tac gag tgc ctg tgc ccc gac ggc ttc cag ctg gtg gcc     1057
125 Lys Ile Gly Tyr Glu Cys Leu Cys Pro Asp Gly Phe Gln Leu Val Ala
126         335             340             345
128 cag cga aga tgc gaa gat atc gat gag tgt cag gat ccc gac acc tgc     1105
129 Gln Arg Arg Cys Glu Asp Ile Asp Glu Cys Gln Asp Pro Asp Thr Cys
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130     350                   355                  360
132 agc cag ctc tgc gtg aac ctg gag ggt ggc tac aag tgc cag tgt gag    1153
133 Ser Gln Leu Cys Val Asn Leu Glu Gly Gly Tyr Lys Cys Gln Cys Glu
134 365                   370                  375              380
136 gaa ggc ttc cag ctg gac ccc cac acg aag gcc tgc aag gct gtg gtc    1201
137 Glu Gly Phe Gln Leu Asp Pro His Thr Lys Ala Cys Lys Ala Val Val
138                   385                  390              395
140 cct gat aaa act gtg aga tgg tgt gca gtg tcg gag cat gag gcc act    1249
141 Pro Asp Lys Thr Val Arg Trp Cys Ala Val Ser Glu His Glu Ala Thr
142             400               405              410
144 aag tgc cag agt ttc cgc gac cat atg aaa agc gtc att cca tcc gat    1297
145 Lys Cys Gln Ser Phe Arg Asp His Met Lys Ser Val Ile Pro Ser Asp
146         415               420              425
148 ggt ccc agt gtt gct tgt gtg aag aaa gcc tcc tac ctt gat tgc atc    1345
149 Gly Pro Ser Val Ala Cys Val Lys Lys Ala Ser Tyr Leu Asp Cys Ile
150     430               435              440
152 agg gcc att gcg gca aac gaa gcg gat gct gtg aca ctg gat gca ggt    1393
153 Arg Ala Ile Ala Ala Asn Glu Ala Asp Ala Val Thr Leu Asp Ala Gly
154 445               450              455              460
156 ttg gtg tat gat gct tac ttg gct ccc aat aac ctg aag cct gtg gtg    1441
157 Leu Val Tyr Asp Ala Tyr Leu Ala Pro Asn Asn Leu Lys Pro Val Val
158             465               470              475
160 gca gag ttc tat ggg tca aaa gag gat cca cag act ttc tat tat gct    1489
161 Ala Glu Phe Tyr Gly Ser Lys Glu Asp Pro Gln Thr Phe Tyr Tyr Ala
162         480               485              490
164 gtt gct gtg gtg aag aag gat agt ggc ttc cag atg aac cag ctt cga    1537
165 Val Ala Val Val Lys Lys Asp Ser Gly Phe Gln Met Asn Gln Leu Arg
166     495               500              505
168 ggc aag aag tcc tgc cac acg ggt cta ggc agg tcc gct ggg tgg aac    1585
169 Gly Lys Lys Ser Cys His Thr Gly Leu Gly Arg Ser Ala Gly Trp Asn
170     510               515              520
172 atc ccc ata ggc tta ctt tac tgt gac tta cct gag cca cgt aaa cct    1633
173 Ile Pro Ile Gly Leu Leu Tyr Cys Asp Leu Pro Glu Pro Arg Lys Pro
174 525               530              535              540
176 ctt gag aaa gca gtg gcc aat ttc ttc tcg ggc agc tgt gcc cct tgt    1681
177 Leu Glu Lys Ala Val Ala Asn Phe Phe Ser Gly Ser Cys Ala Pro Cys
178             545               550              555
180 gcg gat ggg acg gac ttc ccc cag ctg tgt caa ctg tgt cca ggg tgt    1729
181 Ala Asp Gly Thr Asp Phe Pro Gln Leu Cys Gln Leu Cys Pro Gly Cys
182             560               565              570
184 ggc tgc tcc acc ctt aac caa tac ttc ggc tac tcg gga gcc ttc aag    1777
185 Gly Cys Ser Thr Leu Asn Gln Tyr Phe Gly Tyr Ser Gly Ala Phe Lys
186     575               580              585
188 tgt ctg aag gat ggt gct ggg gat gtg gcc ttt gtc aag cac tcg act    1825
189 Cys Leu Lys Asp Gly Ala Gly Asp Val Ala Phe Val Lys His Ser Thr
190     590               595              600
192 ata ttt gag aac ttg gca aac aag gct gac agg gac cag tat gag ctg    1873
193 Ile Phe Glu Asn Leu Ala Asn Lys Ala Asp Arg Asp Gln Tyr Glu Leu
194 605               610              615              620
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196 ctt tgc cta gac aac acc cgg aag ccg gta gat gaa tac aag gac tgc      1921
197 Leu Cys Leu Asp Asn Thr Arg Lys Pro Val Asp Glu Tyr Lys Asp Cys
198              625              630              635
200 cac ttg gcc cag gtc cct tct cat acc gtc gtg gcc cga agt atg ggc      1969
201 His Leu Ala Gln Val Pro Ser His Thr Val Val Ala Arg Ser Met Gly
202              640              645              650
204 ggc aag gag gac ttg atc tgg gag ctt ctc aac cag gcc cag gaa cat      2017
205 Gly Lys Glu Asp Leu Ile Trp Glu Leu Leu Asn Gln Ala Gln Glu His
206          655              660              665
208 ttt ggc aaa gac aaa tca aaa gaa ttc caa cta ttc agc tct cct cat      2065
209 Phe Gly Lys Asp Lys Ser Lys Glu Phe Gln Leu Phe Ser Ser Pro His
210      670              675              680
212 ggg aag gac ctg ctg ttt aag gac tct gcc cac ggg ttt tta aaa gtc      2113
213 Gly Lys Asp Leu Leu Phe Lys Asp Ser Ala His Gly Phe Leu Lys Val
214 685              690              695              700
216 ccc cca agg atg gat gcc aag atg tac ctg ggc tat gag tat gtc act      2161
217 Pro Pro Arg Met Asp Ala Lys Met Tyr Leu Gly Tyr Glu Tyr Val Thr
218              705              710              715
220 gcc atc cgg aat cta cgg gaa ggc aca tgc cca gaa gcc cca aca gat      2209
221 Ala Ile Arg Asn Leu Arg Glu Gly Thr Cys Pro Glu Ala Pro Thr Asp
222              720              725              730
224 gaa tgc aag cct gtg aag tgg tgt gcg ctg agc cac cac gag agg ctc      2257
225 Glu Cys Lys Pro Val Lys Trp Cys Ala Leu Ser His His Glu Arg Leu
226          735              740              745
228 aag tgt gat gag tgg agt gtt aac agt gta ggg aaa ata gag tgt gta      2305
229 Lys Cys Asp Glu Trp Ser Val Asn Ser Val Gly Lys Ile Glu Cys Val
230      750              755              760
232 tca gca gag acc acc gaa gac tgc atc gcc aag atc atg aat gga gaa      2353
233 Ser Ala Glu Thr Thr Glu Asp Cys Ile Ala Lys Ile Met Asn Gly Glu
234 765              770              775              780
236 gct gat gcc atg agc ttg gat gga ggg ttt gtc tac ata gcg ggc aag      2401
237 Ala Asp Ala Met Ser Leu Asp Gly Gly Phe Val Tyr Ile Ala Gly Lys
238              785              790              795
240 tgt ggt ctg gtg cct gtc ttg gca gaa aac tac aat aag agc gat aat      2449
241 Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr Asn Lys Ser Asp Asn
242              800              805              810
244 tgt gag gat aca cca gag gca ggg tat ttt gct gta gca gtg gtg aag      2497
245 Cys Glu Asp Thr Pro Glu Ala Gly Tyr Phe Ala Val Ala Val Val Lys
246          815              820              825
248 aaa tca gct tct gac ctc acc tgg gac aat ctg aaa ggc aag aag tcc      2545
249 Lys Ser Ala Ser Asp Leu Thr Trp Asp Asn Leu Lys Gly Lys Lys Ser
250      830              835              840
252 tgc cat acg gca gtt ggc aga acc gct ggc tgg aac atc ccc atg ggc      2593
253 Cys His Thr Ala Val Gly Arg Thr Ala Gly Trp Asn Ile Pro Met Gly
254 845              850              855              860
256 ctg ctc tac aat aag atc aac cac tgc aga ttt gat gaa ttt ttc agt      2641
257 Leu Leu Tyr Asn Lys Ile Asn His Cys Arg Phe Asp Glu Phe Phe Ser
258              865              870              875
260 gaa ggt tgt gcc cct ggg tct aag aaa gac tcc agt ctc tgt aag ctg      2689
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261 Glu Gly Cys Ala Pro Gly Ser Lys Lys Asp Ser Ser Leu Cys Lys Leu
262             880             885             890
264 tgt atg ggc tca ggc cta aac ctg tgt gaa ccc aac aac aaa gag gga        2737
265 Cys Met Gly Ser Gly Leu Asn Leu Cys Glu Pro Asn Asn Lys Glu Gly
266         895             900             905
268 tac tac ggc tac aca ggc gct ttc agg tgt ctg gtt gag aag gga gat        2785
269 Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Val Glu Lys Gly Asp
270     910             915             920
272 gtg gcc ttt gtg aaa cac cag act gtc cca cag aac act ggg gga aaa        2833
273 Val Ala Phe Val Lys His Gln Thr Val Pro Gln Asn Thr Gly Gly Lys
274 925             930             935             940
276 aac cct gat cca tgg gct aag aat ctg aat gaa aaa gac tat gag ttg        2881
277 Asn Pro Asp Pro Trp Ala Lys Asn Leu Asn Glu Lys Asp Tyr Glu Leu
278             945             950             955
280 ctg tgc ctt gat ggt acc agg aaa cct gtg gag gag tat gcg aac tgc        2929
281 Leu Cys Leu Asp Gly Thr Arg Lys Pro Val Glu Glu Tyr Ala Asn Cys
282             960             965             970
284 cac ctg gcc aga gcc ccg aat cac gct gtg gtc aca cgg aaa gat aag        2977
285 His Leu Ala Arg Ala Pro Asn His Ala Val Val Thr Arg Lys Asp Lys
286         975             980             985
288 gaa gct tgc gtc cac aag ata tta cgt caa cag cag cac cta ttt gga        3025
289 Glu Ala Cys Val His Lys Ile Leu Arg Gln Gln Gln His Leu Phe Gly
290     990             995             1000
292 agc aac gta act gac tgc tcg ggc aac ttt tgt ttg ttc cgg tcg gaa        3073
293 Ser Asn Val Thr Asp Cys Ser Gly Asn Phe Cys Leu Phe Arg Ser Glu
294 1005            1010            1015            1020
296 acc aag gac ctt ctg ttc aga gat gac aca gta tgt ttg gcc aaa ctt        3121
297 Thr Lys Asp Leu Leu Phe Arg Asp Asp Thr Val Cys Leu Ala Lys Leu
298             1025            1030            1035
300 cat gac aga aac aca tat gaa aaa tac tta gga gaa gaa tat gtc aag        3169
301 His Asp Arg Asn Thr Tyr Glu Lys Tyr Leu Gly Glu Glu Tyr Val Lys
302             1040            1045            1050
304 gct gtt ggt aac ctg aga aaa tgc tcc acc tca tca ctc ctg gaa gcc        3217
305 Ala Val Gly Asn Leu Arg Lys Cys Ser Thr Ser Ser Leu Leu Glu Ala
306         1055            1060            1065
308 tgc act ttc cgt aga cct taaaatctca gaggtagggc tgccaccaag              3265
309 Cys Thr Phe Arg Arg Pro
310     1070
312 gtgaagatgg gaacgcagat gatccatgag tttgccctgg tttcactggc ccaagtggtt      3325
313 tgtgctaacc acgtctgtct tcacagctct gtgttgccat gtgtgctgaa caaaaaataa      3385
314 aaattattat tgattttata tttcggggg ggggctgcag ccc                        3428
316 <210> SEQ ID NO: 2
317 <211> LENGTH: 1074
318 <212> TYPE: PRT
319 <213> ORGANISM: Homo sapiens
321 <400> SEQUENCE: 2
322 Met Gly Pro Trp Gly Trp Lys Leu Arg Trp Thr Val Ala Leu Leu Leu
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324 Ala Ala Ala Gly Thr Ala Val Gly Asp Arg Cys Glu Arg Asn Glu Phe
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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date